AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of claims

1. (Currently amended) A method ~~for~~ of identifying ~~an individual who has~~ a human having an altered risk for developing ~~an autoimmune disease~~ an autoantibody-positive autoimmune disease, comprising detecting the presence of a single nucleotide polymorphism (SNP) ~~as represented by a nucleotide sequence selected from the group consisting~~ at position 101 of SEQ ID ~~NOs~~ NO: 36673~~, 34836, 30710, 13392, 20612,~~ 30382~~, 32827, 29676, 35519, 11389~~ or its complement thereof in said ~~individual's~~ human's nucleic acids, wherein the presence of the SNP is ~~correlated with~~ indicative of an altered risk for ~~autoimmune disease~~ developing said autoantibody-positive autoimmune disease in said human.

2. - 26. (Canceled)

27. (New) The method of claim 1 in which said autoantibody-positive autoimmune disease is selected from the group consisting of rheumatoid arthritis (RA), systemic lupus erythematosus, type 1 diabetes mellitus, Graves disease, and thyroiditis.

28. (New) The method of claim 1 in which said autoantibody-positive autoimmune disease is RF-positive rheumatoid arthritis (RA).

29. (New) The method of claim 1 in which SEQ ID NO: 36673 is contained within the genomic sequence of PTPN22 gene as represented by SEQ ID NO: 10739.

30. (New) The method of claim 1 in which the SNP to be detected is located at position 42798 of SEQ ID NO: 10739.

31. (New) The method of claim 1 in which said human's nucleic acids are extracted from a biological sample therefrom.

32. (New) The method of claim 28 in which said biological sample is blood.

33. (New) The method of claim 1 in which said human's nucleic acids are amplified before the detection is carried out.

34. (New) The method of claim 1 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

35. (New) The method of claim 1 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

36. (New) A method of identifying a human having an increased risk for developing an autoantibody-positive autoimmune disease, comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 36673 or its complement thereof in said human's nucleic acids, wherein the presence of the SNP is indicative of an increased risk for developing said autoantibody-positive autoimmune disease in said human.

37. (New) The method of claim 36 in which said autoantibody-positive autoimmune disease is selected from the group consisting of rheumatoid arthritis (RA), systemic lupus erythematosus, type 1 diabetes mellitus, Graves disease, and thyroiditis.

38. (New) The method of claim 36 in which said autoantibody-positive autoimmune disease is RF-positive rheumatoid arthritis (RA).

39. (New) The method of claim 36 in which SEQ ID NO: 36673 is contained within the genomic sequence of PTPN22 gene as represented by SEQ ID NO: 1688.

40. (New) The method of claim 36 in which the SNP to be detected is located at position 42798 of SEQ ID NO: 10739.

41. (New) The method of claim 36 in which said human's nucleic acids are extracted from a biological sample therefrom.

42. (New) The method of claim 41 in which said biological sample is blood.

43. (New) The method of claim 36 in which said human's nucleic acids are amplified before the detection is carried out.

44. (New) The method of claim 36 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

45. (New) The method of claim 36 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

46. (New) A method of identifying a human having a decreased risk for developing an autoantibody-positive autoimmune disease, comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 36673 or its complement thereof in said human's nucleic acids, wherein the presence of C at position 101 of SEQ ID NO: 36673 is indicative of a decreased risk for said autoantibody-positive autoimmune disease in said human.

47. (New) The method of claim 46 in which said autoantibody-positive autoimmune disease is selected from the group consisting of rheumatoid arthritis (RA), systemic lupus erythematosus, type 1 diabetes mellitus, Graves disease, and thyroiditis.

48. (New) The method of claim 46 in which said autoantibody-positive autoimmune disease is RF-positive rheumatoid arthritis (RA).

49. (New) The method of claim 46 in which SEQ ID NO: 36673 is contained within the genomic sequence of PTPN22 gene as represented by SEQ ID NO: 10739.

50. (New) The method of claim 46 in which the SNP to be detected is located at position 42798 of SEQ ID NO: 10739.

51. (New) The method of claim 46 in which said human's nucleic acids are extracted from a biological sample therefrom.

52. (New) The method of claim 51 in which said biological sample is blood.

53. (New) The method of claim 46 in which said human's nucleic acids are amplified before the detection is carried out.

54. (New) The method of claim 46 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

55. (New) The method of claim 46 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

56. (New) A method of determining a human's risk for developing an autoantibody-positive autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 36673 or its complement thereof in said human's nucleic acids, wherein the presence of T at position 101 of SEQ ID NO: 36673 is indicative of an increased risk for said autoantibody-positive autoimmune disease in said human, or, the presence of C at position 101 of SEQ ID NO: 36673 is indicative of a decreased risk for developing said autoantibody-positive autoimmune disease in said human.

57. (New) The method of claim 56 in which said autoantibody-positive autoimmune disease is selected from the group consisting of rheumatoid arthritis (RA), systemic lupus erythematosus, type 1 diabetes mellitus, Graves disease, and thyroiditis.

58. (New) The method of claim 56 in which said autoantibody-positive autoimmune disease is RF-positive rheumatoid arthritis (RA).

59. (New) The method of claim 56 in which SEQ ID NO: 36673 is contained within the genomic sequence of PTPN22 gene as represented by SEQ ID NO: 10739.

60. (New) The method of claim 56 in which the SNP to be detected is located at position 42798 of SEQ ID NO: 10739.

61. (New) The method of claim 56 in which said human's nucleic acids are extracted from a biological sample therefrom.

62. (New) The method of claim 61 in which said biological sample is blood.

63. (New) The method of claim 56 in which said human's nucleic acids are amplified before the detection is carried out.

64. (New) The method of claim 56 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

65. (New) The method of claim 56 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.